



NOV 8 5 2000

TECH CENTER 1600/2900

2.44



## SEQUENCE LISTING

1

<110> Anderson, Christen M. Davis, Robert E. Clevenger, William Wiley, Sandra Elleen Willer, Scott W. Szabo, Tomas R. Ghosh, Soumitra S. RIZES PRODUCTION OF ADENINE NUCLEOTICE TRANSLOCATOR (ANT), MOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR <130 > 660088.420 <140 × US 09/185, 904 141 - 1998-11-1\* <1600 33 <170 - FastSEQ for Windows Version 3.0 <2100-1 211 - 5 44 112 - 1112 sals Hemo supier <4.00 + 1atgriftgatu adgettgdag off estadag Hactiestgi Scripgderut edelepstyro 12.0 qtotocaaqa ocqoqqtoqo boodatoqaq aqqqtoaaan tqotqotqoa qqtocaqdat 180 qobaqbaaan agatcaqtqo tdaqaadhaq tacaaaqqqa tcattqatto fotqqtqada atocchaaqq agnaqqqctt cototoctto tqqaqqqqta acm.qqccaa ngtqatocqt 243 300 tacticecca eccaagetet caacticore ticaaggara agradaagda gotelletta ggggtgtqy atoggeataa qeaqitetig eyetantiti etqqtaacet qeqteegqt 360 420 ggggeegetg gggeeacete cetttgettt gtetaceege tggaetttge taggaecagg 4 = 0 ttqqotqotq atqtqqqeaq qoqoqooraq riqtqaqttoc atqqtotqqqq cqaotqtato atcaaqater teaaqtetga tggentgagg gggetetaec agggttteaa egteretgte 540 600 caaqqqqatca ttatctataq agctqcctac ttcgqaqtct atgatactgc raaqqqqqtq ongo ngawi o wagasagni yoa wattitti gngagatgga tgattqilosa qagiqigaliy. Et. quaglogeag gyotgotyto otachoofft gacastytto gtoqtagaat gafgafghag tunggingga aaggggunga tattatytal anggggabag tidabi pitg gaggaagatt praasigang auggageraa ggenttentre alaggingent gytenaatgt getgagagan Producing officialist ook attifat standadat is aaasatatgt staa - 4 9.44 ×210 × 2 . 211 - 447 4212 - DNA +213 · Homo sapiet uningu na gazh di chindiogaith gach comhang chaeag Galacht Colonia di chaiddh dda'adh i dda'i haidd ni abizt intalada, indeptogot agen iprin hat englag lengggt eraðader ibgent dett engall det detagenati. 120 dinga praagin agat mantigo lagat aagmaalitanaaa boo ittata bantu list qibbinib

at ti norma del lag maggalagti i tilber i nitter i tipere negro a laci di perchaelit discribitadia. factificenta confagget of faactifitae titocauaatata äafa caaqoa Gafetticit j

```
360
iggtiggtigtigg acaagagaac ocagtittigg ogctactitig cagggaatot ggcatogggt
ggtgddgdag gggddadaic deigtgtitt gtgtadddi tigaittifgd ddgtadddgi
                                                                         420
                                                                         480
chagcagetq atgligggtaa agentgqaqet gaaagggaat teeqagqeet eggtgaetge
                                                                         540
ctggttaaga totacaaate tgatgggatt aagggeetgt accaeggett faacqtgtet
                                                                         600
gligoaquqta ffateafota cogaqooqoo taottogqta totatqacao tqcaaaqqqa
atgetteegg ateccaagaa caeteacate greateaget ggargatege acagactgte
                                                                         660
                                                                         720
actgotgttg cogggttgac ttoctatoca tttgacacog ttogocgcog catgatgatg
                                                                         780
cagteagage geaaaggaae tgacateatg tacacaggea egettgactg etggeggaag
                                                                         840
attgotogtg atgaaggagg caaagottit ticaagggtg catggtocaa tgttotoaga
                                                                         897
ggdatgggtg gtgcttttgt geftgtettg tatgatgaaa teaagaagta cacafaa.
      ₹2105 3
      <211 ≥ 897
      <212 - DNA
      <213 > Hemo sapien
      < 4000 h 3
anganggaan aggocatice citingchaaa daothibhigg ciggaggcal cgiciphig m
atorocaaqa oyyelgtigan focuatogag ogqqtcaaqo figotigoligica qqtimaqcan
                                                                         120
geragnaage agatejroge egakaagnag tabaagggea togtggantg battytoogr
                                                                         180
af secretagy ageography quitatestic ty yaggygen accitiquesa systemitege.
                                                                         2.40
tauturosca oficaaquust caautrogus tisaaggata agtacaagca gatettistta.
                                                                         <0.00 € F
                                                                         36,0
grappy flag amaagracan deadti tiga adgiacittig egggeaansi gyericegys.
420
utigeragung adijinggaal itoangista gujegojaat toungaraust, gijuagad je -
                                                                         480
otggtgaaga tuabbaagto oganggbath nggggbotgt abbaggghti hagtdtotor.
                                                                         540
                                                                         600
gtgcagggea tratcatiota dogggegges tartteggeg ligtacgata: ggccaaggge
                                                                         660
atgeteedeu acceeaagaa cacyeacate qfggtdaget ggatgafege deagaeegfg.
                                                                         720
acqqqqqtqq coqqqqtqqt qtcctacccc ttcqacacqq tqcqqcqqqq catqqtqafq.
cagtocgggo gradaggago tgacatcatg tadacgggca cogtogactg ttggaggaag
                                                                         750
atottcagag atgaggggg caaggeette ttcaagggtg egtggtobaa egtectgegg
                                                                         840
ggdatggggg ydgddithgi ghigyiddig tangadgagh ibaagaaggi gaidtaa
                                                                         5 37
      + 210× 4
      + 211> 43
      +2125 5NA
      <2130 Artificial de pience.</p>
      4 22 D x
      H2239 PCR Primer
      \approx 400 \times 4
                                                                          4 4
ttatateten ausabgggig at mogestid gadetteeta laag.
      +216 - 5
      <211 > 43
      +212 + LNA
      +213 · Artificial Sequence
      HZZER ICR primer
     (x,y_1^*,y_2^*) \in \mathcal{C}_{p_1}
tahabaggba oottagadat affbbit bat itoatolaban aa ti
                                                                          43
      2 111 - W
```

+2.11 + 43

```
3212> DNA
      <213> Artificial Sequence
      <220>
      <223> PCR primer
      -400 > 6
                                                                              4.3
fitatatiting aghatqadag atgongotgt groottogon aag
      <210× 7
      <211> 43
      <212> DNA
       <213> Artificial Sequence
       www.FCR primer
turafaggia corrangigh a mitorituat ticatoalan aag
                                                                              43
       21119-43
       2425~\mathrm{PMA}
       213 Artificial Sequence
      RRZZBR PCR primer
      <4005 5
                                                                              43
thatatoreg aghatyaogg aadaggodat ofoottogod aaa
       1210 × 9
      <2.11 \leq 4.4
      <212> DNA
      Kulba Artificial Sequence
      + 223 + PCR primer
      + 450 × 9
tafataquta bettaqauto abettori ma yotogrodia bayq
                                                                              4.4
      - 2115 21
      szlzs DIA
      *213 Artificial Septence
      %Alter despending princt
     \sim 4.36 \times 15
tatopoolahad laatititatoi il
      +219 + 11
      Allie in

- 12 - PMA

- 12 - Artificial Jeganse
```

```
· 220>
      	imes 223 	imes sequencing primer
      <400> 11
cgccaaaaca gccaagct
                                                                                   18
      <210 > 12
      sa11: 45
      √2125 DNA
      -213 - Artificial Sequence
      ∢220≥
      ×2235 Mutagenic oligonucleotide primer
      400 - 12
ggagatggon fullbergtea tellatogin atogingiae again
                                                                                  45
      + \pm 1 \, \mathrm{fig.} \, 1.4
      < 211 × 45
      + 412 + ENA
      - 313 - Artificial Jequence
      3.220 -
      30238 Mutagenic oxigenucleotide primer
      <.400 - 13
                                                                                   45
gatotgtang acgatgacga taagatgacg gawcaggona totor
      +210× 14
      <2115 35
<212 > DNA
      -213: Artificial Sequence
      A PART OF S
      - 223 - PCR primer
      < 400 → 14
                                                                                   35
congggmaat totgatgang gaabaggoba totob
      +310 + 15
+211 + 34
      +.21z + ENA
      -213 - Artificial Sequence
      · 220 ·
      +22f + FCR primer
     - 4 mm - 1%
configgrating automapaits about the fire and the
                                                                                   3.4
      > 2100 \times 160
      +1.11 + 41
      + z1z + i4M
      Switz Artificial Dequence
```

100

<2223 > E	PCR primer	
k400% 1 Stafaggato ca	l6 atgaoggaa caggocatot cottogocaa a	41
<210> 1 <211> 4 <212> E <213: F	41	
√2200 <2230 E	PCR primer	
<100% 1 ttawagaant ot	17 ttagatban ottottgado todfogtaba g	41
#2101 1 #211 1 #222 I #213 2		
220 223 - \$	Compensing primer	
1905 j gaatgataac ca		1.9
+ 210 + 1 + 211 + 1 + 212 + F + 213 + F	19	
220 223 - 3	Tequenoting primer	
१००० । बर्गा एडव्यक्ट्रब स्ट		i M
.10: 2 -211: 1 .12: 1 -213: 7	in	
220 2237 ()	Sequencing primer	
- 400° - 2 - 40° + 1999 21 + 120		1 11
+210+2 +211+1 +212+1 +21*+7	i 4	
1270 s 1223 s s	Despuerterinsk parimeer	

<400° 21 tabggodaag ggdattot	1.8
.2109 22 0211> 18 1212: DNA 0213: Artificial Sequence	
220: -223: Sequencing primer	
:400> 22 igaaqogqaa gitootat	18
czlo. 23 217: 18 212: DNA czlo Artificiał Soquence	
Fig Organizing prime:	
.400. 23 atdooggoto oogtaaga	
:210: 24 :211: 31 :212: DNA :213: Artificial Sequence	
2209 2239 Mutagenio bligonucleotide primer	
idoku 24 gyddyfitho yfostafi ogfodtogtd y	37
tz10× z5 ±11 ÷ 31 ±12 ÷ DNA ÷213 ÷ Artificial Sequence	
North Skill Mutagemic Oligonusidestide primer	
k 400 × 25 Hejaddat qadi gahalagat qali oggaladlagen in	: 1
- 210 26 - 211 - 41 - 212 - ENA - 213 - Artificial Jespience	
-220- -124-17E-primer	
+ <b>4</b> 位 - 4 1.0	

```
41
ttaaaqaatt catgacggaa caggccatct ccttcqccaa a
      <210> 27
      <211: 41
       -212° ENA
      <213> Artificial Sequence
      <1.220>
      <223> FCR primer
      <400> 27
trataggato oftagatoac offettgago fogloglaca g
                                                                            41
      22105-28
       12119 42
       2127 FNA
       0213 - Artificial deduence
       220
       123° FOR Frimer
       400 28
                                                                            42.
ttaatgygta odatgudgda adaggddatu todffogdda aa-
      ~210> 29
      <211: 42</p>
      <2121 DNA
      32132 Artificial Sequence
      <i230 POR primer</pre>
      <4001 29
thatactoga gitagatear chicitgago toglogiara ag
                                                                            -12.
      <210> 30
      <211: 15
      <2125 PRT
      <2135 Artificial Dequence
      . 220 -
      +223 - Wynthetin polypeptide
Cys Trp Arg Lys The The Arg Asp did dry dry Dys Ala Pho The
1 5 10 15
      \leq 210 \leq 31
      +211 \leq 297
      ·zlz- ERI
      exite Hemolecular
      4:1
More Bly Asp His Ala Trp Wer The Leu Lyc Asp The Leu Ala Gly Ala
The Ala Ala Ala Values type The Ala Value From No. 416 Are Value 25
```

```
Lys Leu Leu Gen Val Gin His Ala Ser Lys Gin Ile Ser Ala Glu
                           40
Lys Gin Tyr Lys Gly Ile Ile Asp Cys Val Val Arg Ile Pro Lys Glu
                       55
Gln Gly Phe Leu Ser Phe Trp Arg Gly Asn Leu Ala Asn Val IIe Arg
Tyr Phe Pro Thr Gln Ala Leu Asn Phe Ala Phe Lys Asp Lys Tyr Lys
                                  90
Gln Leu Phe Leu Gly Gly Val Asp Arg His Lys Gln Phe Trp Arg Tyr
          100
                              105
Fhe Ala Giy Ash Leu Ala Ser Gly Gly Ala Ala Gly Ala Thr Ser Leu
    115
                           120
Cys Phe Val Tyr Pro Lou Asp Phe Ala Arg Thr Arg Leu Ala Ala Asp
                    135
                                           140
Val Gly Arg Arg Ala Gln Arg Glu Phe His Gly Leu Gly Asp Cys IIe
The Dys The The Dys Ger Asp Gly Leu Arg Gly Leu Tyr Gln Gly Phe
              165
Ash val Ger Val Gin Gly Ile He He Tyr Arg Ala Ata Tyr Ebo Gly
Val Tyr Asp Thr Ala Lys Gly Met Leu Pro Asp Pro Lys Ash Val His
The Phy Mai Ser Trp Hot ile Ala Gln Ser Mai Thr Ala Mai Ala Gly
                       2.15
hed bed der Tyr Pro Phe Asp Thr Val Ard Ard Ard Med Med Med Glr
Ser Gly Arg Lys Gly Ala Asp Ile Met Tyr Thr Gly Thr Val Asp Cyc
Trp Arg Lys Ile Ala Lys Asp Glu Gly Ala Lys Ala The Phe Lys Gly
                               265
Ala Trp Ser Ash Val Leu Arg Gly Met Gly Gly Ala Phe Val Leu Val
                         280
leu Tyr Asp Glu Ile bys bys Tyr Val
     <210 → 32
     ×211 × 298
     <212 > PRT
     *z13 = Homo sapien
     +400 + 42
Met Thr Asp Ala Ala Leu Ger the Ala Lys Asp Ehe Lea Ala Gly Gly
Val Ala Ala Ara Ile Cor Lys The Ala Val Ala Pro Ile Glu Ari Val
   Lys Glr Tyr Lys Gly lie lie Asp Cys Val Val Arg Ne Pro Lys Glu
Sim Gld Vil Jed Jor the Trp Ard Gly Ash Leu Ala Ash Val Ille Ard
Tyr Phe Pro Thr Sin Ala Led Aso The Ala The Lys Asp bys Tyr Lyc
Sin lie Pho Leu Gly Gly Vai Asp Lys Arm Thr Sin Ebo Trp Arm Tyr
166 - 168 - 188
the Ala Sty Ash hou Ala Ser Sty Gly Ala Ala Sty Ala Thr Fer Lou
```

Cys Phe Val Tyr Pro Leu Asp the Ala Arg Thr Arg Leu Ala Ala Asp 135 130 140 Vai Gly Lys Ala Gly Ala Glu Arg Glu Fhe Arg Gly Leu Gly Asp Cys 150 155 Leu Val Lys Ile Tyr Lys Ser Asp Gly lie Lys Gly Leu Tyr Gln Gly 165 170 Phe Asn Val Ser Val Gln Gly Ile Ile Ile Tyr Arg Ala Ala Tyr Phe 180 185 190 Gly 11e Tyr Asp Thr Ala Lys Gly Met Leu Pro Asp Pro Lys Asn Thr 195 200 205 His lie Val 11s Ser Trp Met 11e Ala Gln Thr Val Thr Ala Val Ala 210 215 Gly Leu Thr Ser Tyr Pro Phe Asp Thr Val Arg Arg Arg Met Met Mot 2.30 2.35 Gln Ser Gly Arg Lys Cly Thr Asp IIe Met Tyr Thr Gly Thr Leu Asp 2.15 Cys Trp Ard Lys Ilo Ala Ard Asp Slu Gly Gly Lys Ala Phe Phe Lys oly Ala Trp Ser Ash Val Leu Ary Gly Met Gly Gly Ala Ehe Tal Leu Yel Lon Tyr Asp Glu lie Lys Lys Tyr Thr

S.211 + 238

- 212 + FRT

- 213 - Home sapien

 $\sim 400 \times 33$ 

Met Thr Glu Gin Ala Ile Ser Phe Ala Lys Asp Phe Leu Ala Gly Cly Tie Ala Ala Ala Ile Ser Lys Thr Ala Val Ala Pro Ile Giu Arg Vai Lys Leu Leu Eeu Gin Val Gin His Ala Jer Lys Gin Lie Ala Ala Asp 200 Lys Gln Tyr Lys Gly Ile Val Asp Cys Ile Val Arg Ile Fro Lys Glu 55 din Gly Mal Leu Ser Phe Trp Arg Gly Ash Leu Ala Ash Mai Ile Arg Tyr Phe Pro Thr Gln Ala Leu asn The Ala Phe Lys Asp Lys Tyr Lys Gir lie Fhe Leu Sly Gly Val Asp Lys His Thr Gir Phe Trp Arq Tyr The Ala Gry Ash Leu Als Ser Gry Gly Ala Ala Gly Ala The Ser Lou tys the Val Tyr Pro Leu Asp the Ala Ard Thr Ard Lew Ala Ala Asp ] < [-140 Val Gly Lys Ser Gly Thr Glu Arg Glu Ehe Ard Gly Leu Gly Asp Cys 150 155 Let Mal Tys The Thr Lys Ser Asp Gly Tle Arg Guy Leu Tyr Gir Gly The Ser Val Ser Val Sir Sty Ilo II- Ilo Tyr Ard Ala Ala Tyr Fre 1000 1986 Bly Val Tyr Asp Thr Ala Lys Gly Met Lea Fre Asp Ero Lys Ash Thr His Tie Val Val Cer Trp Met He Ala Sln Thr Val Thr Ala Val Ala

Gly Val Val Ser Tyr Pro Phe Asp Thr Val Arg Arg Arg Met Met 240
Cln Ser Gly Arg Lys Gly Ala Asp Ile Met Tyr Thr Gly Thr Val Asp
250
Cys Trp Arg Lys Ile Phe Arg Asp Glu Gly Gly Lys Alu Phe Phe Lys
260
Gly Ala Trp Ser Asn Val Leu Arg Gly Met Gly Gly Ala Phe Val Leu
280
Val Leu Tyr Asp Glu Leu Lys Lys Val Ile
290
Cys Tyr Thr Gly Thr Val Asp
255
Cys Trp Arg Lys Ile Phe Arg Asp Glu Gly Gly Lys Alu Phe Phe Lys
265
Z70
Cys Trp Arg Lys Ile Phe Arg Asp Glu Gly Met Gly Gly Ala Phe Val Leu
285
Cys Trp Arg Lys Ile Phe Arg Asp Gly Met Gly Gly Ala Phe Val Leu
280
Cys Trp Arg Lys Ile Phe Arg Asp Gly Met Gly Gly Ala Phe Val Leu
280
Cys Trp Arg Lys Ile Phe Arg Asp Gly Met Gly Gly Ala Phe Val Leu
280
Cys Trp Arg Lys Ile Phe Arg Asp Gly Met Gly Gly Ala Phe Val Leu
280
Cys Trp Arg Lys Ile Phe Arg Asp Gly Met Gly Gly Ala Phe Val Leu
280
Cys Trp Arg Lys Ile Phe Arg Asp Gly Met Gly Gly Ala Phe Val Leu
280
Cys Trp Arg Lys Ile Phe Arg Asp Gly Met Gly Gly Ala Phe Val Leu